

## SEQUENCE LISTING

<110> GOODNOW JR., ROBERT A.  
 MARK, DAVID F.  
 MARTIN, MITCHELL L.  
 ROSINSKI, JAMES A.

<120> SEQUENCE #115 AS A TARGET FOR IDENTIFYING WEIGHT  
 MODULATING COMPOUNDS

<130> 21366 US1

<140> 10/735,991

<141> 2003-12-15

<150> 60/436,375

<151> 2002-12-23

<160> 6

<170> PatentIn Ver. 3.3

<210> 1

<211> 1014

<212> DNA

<213> Mus musculus

<400> 1

```

atgaactcgt gggacgcggg cctggcgggg ctgctggtgg gcactatcgg cgtgtcgctg 60
ctgtccaacg ggctgggtgct gctctgcctc ctgcacagcg ctgacatccg ccgccaggcg 120
ccggcgctct tcaactctcaa cctcacgtgt ggcaacctgc tgtgtaccgt ggtcaacatg 180
ccactaacac tggccggcgt cgtggcacaa cggcagccgg ccggggaccg cctgtgccgc 240
ctggccgcct tctctgacac ctttctggcc gccaaactcca tgctcagcat ggccgcgctc 300
agcatcgacc gctgggtggc tgtgggtctt ccgctgagct accgtgccaa gatgcgcctc 360
cgagatgccg ctttcatggt ggcctacacg tggctgcacg cgctcacctt ccgggccacc 420
gcgctcgccc tgtcctggct cggcttccac cagctatatg cctcgtgcac actgtgcagc 480
cggcgggccg acgagcgctt gcgctttgct gtcttcacca gcgccttcca tgcgctcagc 540
ttcctgctct ctttcatcgt gctctgcttc acgtacctca aggtgctcaa ggtggcccgc 600
ttccactgca agcgcacgca cgtgatcacc atgcagacgc ttgtgctgtt ggtggacata 660
caccaccagt tgaggggaac gtgtctggag gaacagaagc ggagggcgaca gcgtgccacc 720
aagaagatca gcaccttcat agggaccttc cttgtgtgct ttgcacccta tgtgattacc 780
aggctgggtg aactcttctc cacagcacc attggctctc actggggagt gctgtccaag 840
tgcttggcct acagcaaggc cgcttctgac cccttcgtgt attccttgct gcgacaccaa 900
taccgcagga gctgcaagga gctcctgaac aggatcttca acagacgctc ctttcaactc 960
gtgggcctca caggtgactc tcacagccag aacattctgc cagtgtcgga atga 1014

```

<210> 2

<211> 337

<212> PRT

<213> Mus musculus

<400> 2

```

Met Asn Ser Trp Asp Ala Gly Leu Ala Gly Leu Leu Val Gly Thr Ile
  1                      5                      10                      15

Gly Val Ser Leu Leu Ser Asn Gly Leu Val Leu Leu Cys Leu Leu His
                20                      25                      30

```

Ser Ala Asp Ile Arg Arg Gln Ala Pro Ala Leu Phe Thr Leu Asn Leu  
                   35                                  40                                  45  
 Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu  
           50                                  55                                  60  
 Ala Gly Val Val Ala Gln Arg Gln Pro Ala Gly Asp Arg Leu Cys Arg  
   65                                  70                                  75                                  80  
 Leu Ala Ala Phe Leu Asp Thr Phe Leu Ala Ala Asn Ser Met Leu Ser  
                                   85                                  90                                  95  
 Met Ala Ala Leu Ser Ile Asp Arg Trp Val Ala Val Val Phe Pro Leu  
                   100                                  105                                  110  
 Ser Tyr Arg Ala Lys Met Arg Leu Arg Asp Ala Ala Phe Met Val Ala  
                   115                                  120                                  125  
 Tyr Thr Trp Leu His Ala Leu Thr Phe Pro Ala Thr Ala Leu Ala Leu  
           130                                  135                                  140  
 Ser Trp Leu Gly Phe His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser  
   145                                  150                                  155                                  160  
 Arg Arg Pro Asp Glu Arg Leu Arg Phe Ala Val Phe Thr Ser Ala Phe  
                                   165                                  170                                  175  
 His Ala Leu Ser Phe Leu Leu Ser Phe Ile Val Leu Cys Phe Thr Tyr  
                   180                                  185                                  190  
 Leu Lys Val Leu Lys Val Ala Arg Phe His Cys Lys Arg Ile Asp Val  
           195                                  200                                  205  
 Ile Thr Met Gln Thr Leu Val Leu Leu Val Asp Ile His Pro Ser Val  
           210                                  215                                  220  
 Arg Glu Arg Cys Leu Glu Glu Gln Lys Arg Arg Arg Gln Arg Ala Thr  
   225                                  230                                  235                                  240  
 Lys Lys Ile Ser Thr Phe Ile Gly Thr Phe Leu Val Cys Phe Ala Pro  
                                   245                                  250                                  255  
 Tyr Val Ile Thr Arg Leu Val Glu Leu Phe Ser Thr Ala Pro Ile Gly  
                   260                                  265                                  270  
 Ser His Trp Gly Val Leu Ser Lys Cys Leu Ala Tyr Ser Lys Ala Ala  
           275                                  280                                  285  
 Ser Asp Pro Phe Val Tyr Ser Leu Leu Arg His Gln Tyr Arg Arg Ser  
           290                                  295                                  300  
 Cys Lys Glu Leu Leu Asn Arg Ile Phe Asn Arg Arg Ser Leu His Ser  
   305                                  310                                  315                                  320  
 Val Gly Leu Thr Gly Asp Ser His Ser Gln Asn Ile Leu Pro Val Ser  
                   325                                  330                                  335

Glu

<210> 3  
 <211> 1172  
 <212> DNA  
 <213> Rattus norvegicus

<400> 3  
 ctgaacgccca tcagcgggcg cgcaccatga actcgtggga cgcgggcctg gcggggctgc 60  
 tgggtgggcac aatcggcggtg tcgctgctgt ccaacgggct ggtgctgctc tgcctcctgc 120  
 acagcgctga catccgccgc caggcgccgg cgctcttcac tctcaacctc acgtgtggca 180  
 acctgctgtg taccgtgggtc aacatgccac taacactggc cggcgctcgtg gcacaacggc 240  
 agccggccgg ggaccgcctg tgccgcctgg ccgccttcct cgacaccttt ctggccgccca 300  
 actccatgct cagtatggcc gcgctcagca tcgaccgctg ggtggctgtg gtcttcccg 360  
 tgagctaccg tgccaagatg cgcctccgag atgcgcctt catggtggcc tacacgtggc 420  
 tgacgcgct caccctcccg gccaccgcgc tcgcctgtc ctggctcggc ttccaccagc 480  
 tgtatgcctc gtgcacgctg tgcagccggc ggcccgaaga gcgcctgcgc tttgctgtct 540  
 tcaccagcgc cttccatgcg cttagcttcc tgctctcctt catcgtgctc tgcttcacgt 600  
 acctcaaggt gctcaaggtg gcccgtttcc actgcaagcg catcgacgtg atcaccatgc 660  
 agacgctcgt gctgttagtg gacatccatc ccagtgtgag ggaacgatgt ctggaggaaac 720  
 agaagcggag gcggcagcgt gccaccaaga agatcagcac cttcataggg accttcctcg 780  
 tgtgttttgc accctatgtg attaccaggc tgggtggaact cttctccaca gcacccattg 840  
 actcacactg ggggtgtgctg tccaagtgtc tggcctacag caaggctgct tctgaccctc 900  
 tcgtgtactc cttgctgcga caccagtacc gcaggagctg caaggagctt ctgaacagga 960  
 tcttcaacag acgctccatt cactctgtgg gcctcacagg tgactctcac agccagaaca 1020  
 ttctgccagt gtcggaatga aggacagctc tcctgttggg gaggttcagaa tgaggtggcc 1080  
 agagcagagg gaggtggtct gggactcctg ggtggacagg aactgccacc attgtctggc 1140  
 gattgacatg atgctgatgt ctgaacaaga tc 1172

<210> 4  
 <211> 337  
 <212> PRT  
 <213> Rattus norvegicus

<400> 4  
 Met Asn Ser Trp Asp Ala Gly Leu Ala Gly Leu Leu Val Gly Thr Ile  
 1 5 10 15  
 Gly Val Ser Leu Leu Ser Asn Gly Leu Val Leu Leu Cys Leu Leu His  
 20 25 30  
 Ser Ala Asp Ile Arg Arg Gln Ala Pro Ala Leu Phe Thr Leu Asn Leu  
 35 40 45  
 Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu  
 50 55 60  
 Ala Gly Val Val Ala Gln Arg Gln Pro Ala Gly Asp Arg Leu Cys Arg  
 65 70 75 80  
 Leu Ala Ala Phe Leu Asp Thr Phe Leu Ala Ala Asn Ser Met Leu Ser  
 85 90 95  
 Met Ala Ala Leu Ser Ile Asp Arg Trp Val Ala Val Val Phe Pro Leu  
 100 105 110

Ser Tyr Arg Ala Lys Met Arg Leu Arg Asp Ala Ala Phe Met Val Ala  
           115                          120                          125  
 Tyr Thr Trp Leu His Ala Leu Thr Phe Pro Ala Thr Ala Leu Ala Leu  
           130                          135                          140  
 Ser Trp Leu Gly Phe His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser  
   145                          150                          155                          160  
 Arg Arg Pro Asp Glu Arg Leu Arg Phe Ala Val Phe Thr Ser Ala Phe  
                           165                          170                          175  
 His Ala Leu Ser Phe Leu Leu Ser Phe Ile Val Leu Cys Phe Thr Tyr  
                           180                          185                          190  
 Leu Lys Val Leu Lys Val Ala Arg Phe His Cys Lys Arg Ile Asp Val  
           195                          200                          205  
 Ile Thr Met Gln Thr Leu Val Leu Leu Val Asp Ile His Pro Ser Val  
           210                          215                          220  
 Arg Glu Arg Cys Leu Glu Glu Gln Lys Arg Arg Arg Gln Arg Ala Thr  
   225                          230                          235                          240  
 Lys Lys Ile Ser Thr Phe Ile Gly Thr Phe Leu Val Cys Phe Ala Pro  
                           245                          250                          255  
 Tyr Val Ile Thr Arg Leu Val Glu Leu Phe Ser Thr Ala Pro Ile Asp  
                           260                          265                          270  
 Ser His Trp Gly Val Leu Ser Lys Cys Leu Ala Tyr Ser Lys Ala Ala  
           275                          280                          285  
 Ser Asp Pro Phe Val Tyr Ser Leu Leu Arg His Gln Tyr Arg Arg Ser  
           290                          295                          300  
 Cys Lys Glu Leu Leu Asn Arg Ile Phe Asn Arg Arg Ser Ile His Ser  
   305                          310                          315                          320  
 Val Gly Leu Thr Gly Asp Ser His Ser Gln Asn Ile Leu Pro Val Ser  
                           325                          330                          335

Glu

<210> 5

<211> 1014

<212> DNA

<213> Homo sapiens

<400> 5

atgaactcgt gggacgcggg cctggcgggg ctactggtgg gcacgatggg cgtctcgctg 60  
 ctgtccaacg cgctggtgct gctctgcctg ctgcacagcg cggacatccg ccgccaggcg 120  
 ccggcgctct tcaccctgaa cctcacgtgc gggaacctgc tgtgcaccgt ggtcaacatg 180  
 ccgctcacgc tggccggcgt cgtggcgag cggcagccgg cgggcgaccg cctgtgccgc 240  
 ctggctgect tcctcgacac cttcctggct gccaaactcca tgctcagcat ggccgcgctc 300

```

agcatcgacc gctgggtggc cgtgggtcttc ccgctgagct accggggccaa gatgcgcctc 360
cgcgacgcgg cgctcatggt ggcctacacg tggctgcacg cgctcacctt cccagccgcc 420
gcgctcggcc tgtcctgggt cggcttccac cagctgtacg cctcgtgcac gctgtgcagc 480
cggcgggccag acgagcgctt gcgcttcgcc gtcttcactg gcgccttcca cgtctcagc 540
ttcctgctct ccttcgtcgt gctctgctgc acgtacctca aggtgctcaa ggtggcccgc 600
ttccattgca agcgcacgca cgtgatcacc atgcagacgc tgggtgctgct ggtggacctg 660
caccacagtg tgcgggaacg ctgtctggag gagcagaagc ggaggcgaca gcgagccacc 720
aagaagatca gcaccttcat agggaccttc cttgtgtgct tcgcgcccta tgtgatcacc 780
aggctagtgg agctcttctc cacgggtgcc atcggtctcc actggggggg gctgtccaag 840
tgcttggcgt acagcaaggc cgcacccgac ccctttgtgt actccttact gcgacaccag 900
taccgcaaaa gctgcaagga gattctgaac aggtcctgac acagacgctc catccactcc 960
tctggcctca caggcgactc tcacagccag aacattctgc cgggtgtctga gtga 1014

```

<210> 6

<211> 337

<212> PRT

<213> Homo sapiens

<400> 6

```

Met Asn Ser Trp Asp Ala Gly Leu Ala Gly Leu Leu Val Gly Thr Met
  1              5              10              15

Gly Val Ser Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Leu Leu His
          20              25              30

Ser Ala Asp Ile Arg Arg Gln Ala Pro Ala Leu Phe Thr Leu Asn Leu
      35              40              45

Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu
  50              55              60

Ala Gly Val Val Ala Gln Arg Gln Pro Ala Gly Asp Arg Leu Cys Arg
  65              70              75              80

Leu Ala Ala Phe Leu Asp Thr Phe Leu Ala Ala Asn Ser Met Leu Ser
          85              90              95

Met Ala Ala Leu Ser Ile Asp Arg Trp Val Ala Val Val Phe Pro Leu
      100              105              110

Ser Tyr Arg Ala Lys Met Arg Leu Arg Asp Ala Ala Leu Met Val Ala
      115              120              125

Tyr Thr Trp Leu His Ala Leu Thr Phe Pro Ala Ala Ala Leu Ala Leu
      130              135              140

Ser Trp Leu Gly Phe His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser
      145              150              155              160

Arg Arg Pro Asp Glu Arg Leu Arg Phe Ala Val Phe Thr Gly Ala Phe
          165              170              175

His Ala Leu Ser Phe Leu Leu Ser Phe Val Val Leu Cys Cys Thr Tyr
      180              185              190

Leu Lys Val Leu Lys Val Ala Arg Phe His Cys Lys Arg Ile Asp Val
      195              200              205

```

Ile	Thr	Met	Gln	Thr	Leu	Val	Leu	Leu	Val	Asp	Leu	His	Pro	Ser	Val
210						215					220				
Arg	Glu	Arg	Cys	Leu	Glu	Glu	Gln	Lys	Arg	Arg	Arg	Gln	Arg	Ala	Thr
225					230					235					240
Lys	Lys	Ile	Ser	Thr	Phe	Ile	Gly	Thr	Phe	Leu	Val	Cys	Phe	Ala	Pro
				245					250					255	
Tyr	Val	Ile	Thr	Arg	Leu	Val	Glu	Leu	Phe	Ser	Thr	Val	Pro	Ile	Gly
			260					265					270		
Ser	His	Trp	Gly	Val	Leu	Ser	Lys	Cys	Leu	Ala	Tyr	Ser	Lys	Ala	Ala
		275					280					285			
Ser	Asp	Pro	Phe	Val	Tyr	Ser	Leu	Leu	Arg	His	Gln	Tyr	Arg	Lys	Ser
	290					295					300				
Cys	Lys	Glu	Ile	Leu	Asn	Arg	Leu	Leu	His	Arg	Arg	Ser	Ile	His	Ser
305					310					315					320
Ser	Gly	Leu	Thr	Gly	Asp	Ser	His	Ser	Gln	Asn	Ile	Leu	Pro	Val	Ser
				325					330					335	

Glu